



O I P E

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/077,111

DATE: 03/04/2002
TIME: 14:52:07

Input Set : A:\30534111.app
Output Set: N:\CRF3\03042002\J077111.raw

3 <110> APPLICANT: Todderud, C. Gordon
 4 Finger, Joshua N.
 5 Rillema, Jill
 7 <120> TITLE OF INVENTION: TBA
 9 <130> FILE REFERENCE: 3053-4114US2
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/077,111
 C--> 12 <141> CURRENT FILING DATE: 2002-02-15
 14 <150> PRIOR APPLICATION NUMBER: 60/294,181
 15 <151> PRIOR FILING DATE: 2001-05-29
 17 <150> PRIOR APPLICATION NUMBER: 60/269,366
 18 <151> PRIOR FILING DATE: 2001-02-16
 20 <160> NUMBER OF SEQ ID NOS: 25
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1818
 26 <212> TYPE: DNA
 27 <213> ORGANISM: HUMAN
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 33 ggtgacgtg tcaactgtg tgccttctcc ttttcctct tggctacttg ctccctggac 240
 34 aaaacaattc gcctgtactc gttacgtgac tttactgaac tqccacatcc tccattgaag 300
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 37 atggaacacgc ctatggcag ccctgtgagg gtttgcagg ttccccaga ctccacgtgt 480
 38 ttggcatcag gggcagctga tggaaactgtg gttttgtgga atgcacagtc atacaaatata 540
 39 tatagatgtg gtatgtttaa agatggctcc ttggccgcat gtgcattttc tccaatgg 600
 40 agtttttttgc tcaactggc ttcattgtggt gatttaacag tttggatgaa taaaatgggg 660
 41 tgtctgcata gtaaaaaaagc acatgtatctt ggaattacat gtcgcgattt ttcttcacag 720
 42 ccagtttctg atggagaaca agtgtttcag tttttcgc tggcatcatg tggcaggat 780
 43 tggcaagtc aaattttggat tttttttt acccataatct taggttttga attaaaatata 840
 44 aaaagtacac tgagtggca ctgtgtctt gttctggctt gtgttttccatgtatggg 900
 45 caatgtctat ttcagggttc agtggataag tctgtcatat tatatgataac taataactgag 960
 46 aatataacttc acacattgac tcaagcacacc aggtatgtca caacttgtc ttttgcacat 1020
 47 aatacccttt tacttgcata tggatcaatg gacaaaacag tgaacatctg gcaatttgac 1080
 48 ctggaaacac tttgcacaacg aaggcgccaca gaacatcagc tgaagcaatt taccgaagat 1140
 49 tggcagagg aggtgtctc aacatggctt tggcacaag attaaaaga tcttggat 1200
 50 atttcaaga tgaataacat tggatggaaa gaactgtga atcttacaaa agaaagtctg 1260
 51 gctgatgatt tggatggatgat tggatggatgaa aagtgtgg 1320
 52 gacgtcaggg ccaaggttaa atccctttct tcaggatcc tggatgaaat tataatgtcca 1380
 53 ataactagaq aacttatgaa agatccggtc atcgcatcag atggcttattc atatgaaaag 1440
 54 gaagcaatggg aaaattggat cagcaaaaaag aaacgtacaa gtcccatgac aaatcttgg 1500

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55 cttccttcag cggtaacttac accaaatagg actctgaaaa tggccatcaa tagatggctg 1560
 56 gagacacacc aaaagtaaaa ttgttgatat tgtattattt atattttcag tgatcttatt 1620
 57 tgaatgatt ataggtaaat actaatcaga cattataaa agaaaaacag gaaaaaggta 1680
 58 aacttcttaa atttagttac ctataaaaaat tgtcaatttt cattttttaa aaaacacatg 1740
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 72 Cys Cys Ala Phe Ser Phe Ser Leu Leu Ala Thr Cys Ser Leu Asp Lys
 73 20 25 30
 75 Thr Ile Arg Leu Tyr Ser Leu Arg Asp Phe Thr Glu Leu Pro His Ser
 76 35 40 45
 78 Pro Leu Lys Phe His Thr Tyr Ala Val His Cys Cys Cys Phe Ser Pro
 79 50 55 60
 81 Ser Gly His Ile Leu Ala Ser Cys Ser Thr Asp Gly Thr Thr Val Leu
 82 65 70 75 80
 84 Trp Asn Thr Glu Asn Gly Gln Met Leu Ala Val Met Glu Gln Pro Ser
 85 85 90 95
 87 Gly Ser Pro Val Arg Val Cys Gln Phe Ser Pro Asp Ser Thr Cys Leu
 88 100 105 110
 90 Ala Ser Gly Ala Ala Asp Gly Thr Val Val Leu Trp Asn Ala Gln Ser
 91 115 120 125
 93 Tyr Lys Leu Tyr Arg Cys Gly Ser Val Lys Asp Gly Ser Leu Ala Ala
 94 130 135 140
 96 Cys Ala Phe Ser Pro Asn Gly Ser Phe Phe Val Thr Gly Ser Ser Cys
 97 145 150 155 160
 99 Gly Asp Leu Thr Val Trp Asp Asp Lys Met Arg Cys Leu His Ser Glu
 100 165 170 175
 102 Lys Ala His Asp Leu Gly Ile Thr Cys Cys Asp Phe Ser Ser Gln Pro
 103 180 185 190
 105 Val Ser Asp Gly Glu Gln Gly Leu Gln Phe Phe Arg Leu Ala Ser Cys
 106 195 200 205
 108 Gly Gln Asp Cys Gln Val Lys Ile Trp Ile Val Ser Phe Thr His Ile
 109 210 215 220
 111 Leu Gly Phe Glu Leu Lys Tyr Lys Ser Thr Leu Ser Gly His Cys Ala
 112 225 230 235 240
 114 Pro Val Leu Ala Cys Ala Phe Ser His Asp Gly Gln Met Leu Val Ser
 115 245 250 255
 117 Gly Ser Val Asp Lys Ser Val Ile Val Tyr Asp Thr Asn Thr Glu Asn
 118 260 265 270
 120 Ile Leu His Thr Leu Thr Gln His Thr Arg Tyr Val Thr Thr Cys Ala
 121 275 280 285
 123 Phe Ala Pro Asn Thr Leu Leu Ala Thr Gly Ser Met Asp Lys Thr
 124 290 295 300

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 189 cagatggcta ttcatatgaa aaggaagcaa tggaaaattg gatcaagcaaa aagaaaatgt 1440
 190 caagtcctat gacaaatctt gttcttcctt cagcgtact tacacccaaat aggacttgta 1500
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 201 1 5 10 15
 203 Leu Glu Gly Gly Ser Arg Ala Pro Pro Leu Leu Gln Ala Val Phe Leu
 204 20 25 30
 206 Gln Ile Lys Asn Met Val Lys Leu Ile His Thr Leu Ala Asp His Gly
 207 35 40 45
 209 Asp Asp Val Asn Cys Cys Ala Phe Ser Phe Ser Leu Leu Ala Thr Cys
 210 50 55 60
 212 Ser Leu Asp Lys Thr Ile Arg Leu Tyr Ser Leu Arg Asp Phe Thr Glu
 213 65 70 75 80
 215 Leu Pro His Ser Pro Leu Lys Phe His Thr Tyr Ala Val His Cys Cys
 216 85 90 95
 218 Cys Phe Ser Pro Ser Gly His Ile Leu Ala Ser Cys Ser Thr Asp Gly
 219 100 105 110
 221 Thr Thr Val Leu Trp Asn Thr Glu Asn Gly Gln Met Leu Ala Val Met
 222 115 120 125
 224 Glu Gln Pro Ser Gly Ser Pro Val Arg Val Cys Gln Phe Ser Pro Asp
 225 130 135 140
 227 Ser Thr Cys Leu Ala Ser Gly Ala Ala Asp Gly Thr Val Val Leu Trp
 228 145 150 155 160
 230 Asn Ala Gln Ser Tyr Lys Leu Tyr Arg Cys Gly Ser Val Lys Asp Gly
 231 165 170 175
 233 Ser Leu Ala Ala Cys Ala Phe Ser Pro Asn Gly Ser Phe Phe Val Thr
 234 180 185 190
 236 Gly Ser Ser Cys Gly Asp Leu Thr Val Trp Asp Asp Lys Met Arg Cys
 237 195 200 205
 239 Leu His Ser Glu Lys Ala His Asp Leu Gly Ile Thr Cys Cys Asp Phe
 240 210 215 220
 242 Ser Ser Gln Pro Val Ser Asp Gly Glu Gln Gly Leu Gln Phe Phe Arg
 243 225 230 235 240
 245 Leu Ala Ser Cys Gly Gln Asp Cys Gln Val Lys Ile Trp Ile Val Ser
 246 245 250 255
 248 Phe Thr His Ile Leu Gly Phe Glu Leu Lys Tyr Lys Ser Thr Leu Ser
 249 260 265 270
 251 Gly His Cys Ala Pro Val Leu Ala Cys Ala Phe Ser Arg Asp Gly Gln
 252 275 280 285
 254 Met Leu Val Ser Gly Ser Val Asp Lys Ser Val Ile Val Tyr Asp Thr
 255 290 295 300
 257 Asn Thr Glu Asn Ile Leu His Thr Leu Thr Gln His Thr Arg Tyr Val
 258 305 310 315 320

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260 Thr Thr Cys Ala Phe Ala Pro Asn Thr Leu Leu Leu Ala Thr Gly Ser
 261 325 330 335
 263 Met Asp Lys Thr Val Asn Ile Trp Gln Phe Asp Leu Glu Thr Leu Cys
 264 340 345 350
 266 Gln Ala Arg Arg Thr Glu His Gln Leu Lys Gln Phe Thr Glu Asp Trp
 267 355 360 365
 269 Ser Glu Glu Asp Val Ser Thr Trp Leu Cys Ala Gln Asp Leu Lys Asp
 270 370 375 380
 272 Leu Val Gly Ile Phe Lys Met Asn Asn Ile Asp Gly Lys Glu Leu Leu
 273 385 390 395 400
 275 Asn Leu Thr Lys Glu Ser Leu Ala Asp Asp Leu Lys Ile Glu Ser Leu
 276 405 410 415
 278 Gly Leu Arg Ser Lys Val Leu Arg Lys Ile Glu Glu Leu Arg Thr Lys
 279 420 425 430
 281 Val Lys Ser Leu Ser Ser Gly Ile Pro Asp Glu Phe Ile Cys Pro Ile
 282 435 440 445
 284 Thr Arg Glu Leu Met Lys Asp Pro Val Ile Ala Ser Asp Gly Tyr Ser
 285 450 455 460
 287 Tyr Glu Lys Glu Ala Met Glu Asn Trp Ile Ser Lys Lys Arg Thr
 288 465 470 475 480
 290 Ser Pro Met Thr Asn Leu Val Leu Pro Ser Ala Val Leu Thr Pro Asn
 291 485 490 495
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 303 <213> ORGANISM: HUMAN
 305 <220> FEATURE:
 306 <223> OTHER INFORMATION: 630 bp partial nucleic acid sequence of human
 307 RET16 cDNA
 309 <400> SEQUENCE: 5
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 312 cttcacacat tgacttcagca caccaggatgt gtcacaactt gtgttttgc acctaataacc 180
 313 cttttacttg ctactggttc aatggacaaa acatgtaaatc tctggcaatt tgacctggaa 240
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 315 gaggaggatg ttcacacatg gttttgtgc caagattaa aagatcttgc tggattttc 360
 316 aatgttgcata acattgtatgg aaaagaactg ttgaatctta caaaagaaag tctggctgtat 420
 317 gatttgtggaaa ttgtatcttgc aggttttttttgc agttaatgtgc tgaggaaaat tgaagatgtc 480
 318 aqgarcaagg ttaaaatccct ttcttcagca attctgtatgc aattttatgt tccaataact 540
 319 agaaaacttta tgaaaatccc ggtcatcgtca tcagatggctt attcatatgt aaagggatgca 600
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 328 <400> SEQUENCE: 6
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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs. Replaced Application Number

L:12 M:271 C: Current Filing Date differs. Replaced Current Filing Date